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aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys 35 40 45	144
aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys 50 55 60	192
aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln 65 70 75 80	240
gaa atg cta aaa cct gcc aaġ aat tct agt gct gtg ata caa aga aaa Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys 85 90 95	288
cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100 105 110	336
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acc atc agc act atg acc cca gga cag atc aca tac act gct act tct Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135 140	432
acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro 145 150 155 160	480
cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu 165 170 175	528
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Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser

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Leu Glu Glu Ala Glu Glu Gln

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								gat Asp						144
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PCT/FI2005/050007

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Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser

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cac cgc a His Arg A	gg aaa rg Lys 5	caa Gln	tgc Cys	aaa Lys	gat Asp 40	gga Gly	gaa Glu	gca Ala	gtg Val	aaa Lys 45	gat Asp	aca Thr	tgc Cys	144
aaa aat c Lys Asn L 50	tt cga eu Arg	gct Ala	tgc Cys	tgc Cys 55	att Ile	cca Pro	tcc Ser	aat Asn	gaa Glu 60	gac Asp	cac His	agg Arg	cga Arg	192
gtt cct g Val Pro A 65	cg aca la Thr	tct Ser	ccc Pro 70	aca Thr	ccc Pro	ttg Leu	agt Ser	gac Asp 75	tca Ser	aca Thr	cca Pro	gga Gly	att Ile 80	240
att gat g Ile Asp A	at att sp Ile	tta Leu 85	aca Thr	gta Val	agg Arg	ttc Phe	acg Thr 90	aca Thr	gac Asp	tac Tyr	ttt Phe	gaa Glu 95	gta Val	288
agc agc a Ser Ser L	ag aaa ys Lys 100	gat Asp	atg Met	gtt Val	gaa Glu	gag Glu 105	tct Ser	gag Glu	gcg Ala	gga Gly	agg Arg 110	gga Gly	act Thr	336
gag acc t Glu Thr S 1									tga					372
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Val Ile Pro	gcc tat agt g Ala Tyr Ser G 20	gt gaa aaa aaa tgc ly Glu Lys Lys Cys 25	tgg aac aga tca Trp Asn Arg Ser 30	ggg 96 Gly
cac tgc agg His Cys Arg 3	aaa caa tgc a Lys Gln Cys L	aa gat gga gaa gca ys Asp Gly Glu Ala 40	gtg aaa gat aca Val Lys Asp Thr 45	tgc 144 Cys
aaa aat ctt Lys Asn Leu 50	cga gct tgc t Arg Ala Cys C 5	gc att cca tcc aat ys Ile Pro Ser Asn 5	gaa gac cac agg Glu Asp His Arg 60	cga 192 Arg
gtt cct gcg Val Pro Ala 65	aca tct ccc a Thr Ser Pro T 70	ea ccc ttg agt gac hr Pro Leu Ser Asp 75	tea aca cca gga Ser Thr Pro Gly	att 240 Ile 80
att gat gat Ile Asp Asp	att tta aca g Ile Leu Thr V 85	ta agg ttc acg aca al Arg Phe Thr Thr 90	gac tac ttt gaa Asp Tyr Phe Glu 95	gta 288 Val
Ser Ser Lys	aaa gat atg g Lys Asp Met V 100	tt gaa gag tct gag al Glu Glu Ser Glu 105	gcg gga agg gga Ala Gly Arg Gly 110	act 336 Thr
-		tt cac cat agc tca al His His Ser Ser 120		372
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	Ala Tyr Ser G 20	ly Glu Lys Lys Cys 25	Trp Asn Arg Ser 30	Gly

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 45 35 40 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 60 50 55 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 80 75 70 65 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 90 95 85 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 110 105 100 Glu Thr Ser Leu Pro Asn Val His His Ser Ser 120 115 <210> 45 <211> 20 <212> DNA Artificial Sequence <213> <220> <223> PCR primer <4.00> 45 20 aggttgagta tttgccagac <210> 46 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 46 19 aggacagggg tgagtgata <210> 47 <211> 246 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(246) <223> Coding sequence for the variant human DEFB126 gene <400> 47 48 atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln 15 10 1 96 ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly

25

20

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cta Leu 65	att Ile	atc Ile	ctg Leu	ttt Phe	tct Ser 70	gtg Val	tcc Ser	aga Arg	caa Gln	aga Arg 75	cta Leu	caa Gln	gaa Glu	ttt Phe	caa Gln 80	240
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Leu	Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
Ile	Cys	Lys 35	Lys	Lys	Cys	Lys	Pro 40	Glu	Glu	Met	His	Val 45	Lys	Asn	Gly	
Trp	Ala 50	Met	Cys	Gly	Lys	Gly 55	Thr	Ala	Val	Phe	Gln 60	Leu	Thr	Asp	Val	
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Gln																
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Leu	Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
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cgt Arg 65	gct Ala	aat Asn	tat Tyr	cct Pro	gtt Val 70	ttc Phe	tgt Cys	gtc Val	cag Gln	aca Thr 75	aag Lys	act Thr	aca Thr	aga Arg	att Ile 80	240
tca Ser	aca Thr	gta Val	aca Thr	gca Ala 85	aca Thr	aca Thr	gca Ala	aca Thr	aca Thr 90	act Thr	ttg Leu	atg Met	atg Met	act Thr 95	act Thr	288
gct Ala	tcg Ser	atg Met	tct Ser 100	tcg Ser	atg Met	gct Ala	cct Pro	acc Thr 105	ccc Pro	gtt Val	tct Ser	ccc Pro	act Thr 110	ggt Gly	tga	336
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Leu	Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
Ile	Cys	Lys 35	Lys	Lys	Cys	Lys	Pro 40	Glu	Glu	Met	His	Val 45		Asn	Gly	
Trp	Ala 50	Met	Cys	Gly	Lys	Gln 55	Arg	Asp	Cys	Cys	Val 60	Pro	Ala	Asp	Arg	
Arg 65	Ala	Asn	Tyr	Pro	Val 70	Phe	Cys	Val	Gln	Thr 75	Lys	Thr	Thr	Arg	Ile 80	
Ser	Thr	Val	Thr	Ala 85	Thr	Thr	Ala	Thr	Thr 90	Thr	Leu	Met	Met	Thr 95	Thr	
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27

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<212> PRT

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Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 60

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